



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/808,052
Source: EFWD
Date Processed by STIC: 10/14/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop-Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/808,052

DATE: 10/14/2004

TIME: 11:37:53

Input Set : A:\18989-033US.txt

Output Set: N:\CRF4\10142004\J808052.raw

3 <110> APPLICANT: Blumberg
 5 <120> TITLE OF INVENTION: Methods of Inhibiting Inflammation
 7 <130> FILE REFERENCE: 18989-033
 9 <140> CURRENT APPLICATION NUMBER: 10/808,052
 10 <141> CURRENT FILING DATE: 2004-03-24
 12 <150> PRIOR APPLICATION NUMBER: 60/457,048
 13 <151> PRIOR FILING DATE: 2003-03-24
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 23
 21 <212> TYPE: RNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (22)
 27 <223> OTHER INFORMATION: Wherein n is dT
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <222> LOCATION: (23)
 32 <223> OTHER INFORMATION: Wherein n is dT
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically
 36 synthesized siRNA
 38 <400> SEQUENCE: 1
 W--> 39 aagcucugga acuaccaacg ann 23
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 23
 44 <212> TYPE: RNA
 45 <213> ORGANISM: Artificial Sequence
 47 <220> FEATURE:
 48 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically
 49 synthesized siRNA
 51 <400> SEQUENCE: 2
 W--> 52 ucguugguag uuccagagcu ann 23
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 3392
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Homo sapiens
 60 <400> SEQUENCE: 3
 61 actccctcac tggctgccat tgaaagagtc caattctcag tgactcctag ctgggcactg 60
 62 gatgcagttg aggattgctg gtcaatatga ttcttcttgc tgtgcttttt ctctgcttca 120
 63 ttctctcata ttcagcttct gttaaaggct acacaactgg tctctcatta aataatgacc 180

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\18989-033US.txt

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64 ggctgtacaa gctcacgtac tccactgaag ttcttcttga tcggggcaaa ggaaaactgc 240
65 aagacagcgt gggctaccgc atttccctcca acgtggatgt ggccttacta tggaggaatc 300
66 ctgatgggta tgatgaccag ttgatccaaa taacgatgaa ggatgtaaat gttgaaaatg 360
67 tgaatcagca gagaggagag aagagcatct tcaaaggaaa aagcccatct aaaataatgg 420
68 gaaaggaaaa cttggaagct ctgcaaagac ctacgctcct tcatctaata catggaaagg 480
69 tcaaagagtt ctactcatat caaaatgagg cagtggccat agaaaatatc aagagaggtc 540
70 tggctagcct atttcagaca cagttaagct ctggaaccac caatgaggta gatatctctg 600
71 gaaattgtaa agtgacctac caggctcatc aagacaaagt gatcaaaatt aaggccttgg 660
72 attcatgcaa aatagcgagg tctggattta cgaccccaa tcaggtcttg ggtgtcagtt 720
73 caaaagctac atctgtcacc acctataaga tagaagacag ctttggtata gctgtgcttg 780
74 ctgaagaaac acacaatttt ggactgaatt tcctacaaac cattaagggg aaaatagtat 840
75 cgaagcagaa attagagctg aagacaaccg aagcaggccc aagattgatg tctggaaagc 900
76 aggctgcagc cataatcaaa gcagttgatt caaagtacac ggccattccc attgtggggc 960
77 aggtcttcca gagccactgt aaaggatgtc cttctctctc ggagctctgg cgggccacca 1020
78 ggaaatacct gcagcctgac aacctttcca aggctgaggc tgtcagaaac ttcttgccct 1080
79 tcattcagca cctcaggact gcgaagaaag aagagatcct tcaaatacta aagatggaaa 1140
80 ataaggaagt attacctcag ctggtggatg ctgtcacctc tgctcagacc tcagactcat 1200
81 tagaagccat tttggacttt ttggatttca aaagtgcagc cagcattatc ctccaggaga 1260
82 ggtttctcta tgctgtgga ttgcttctc atcccaatga agaactctg agagccctca 1320
83 ttagtaagtt caaaggttct attggtacga gtgacatcag agaaactgtt atgatcatca 1380
84 ctgggacact tgtcagaaag ttgtgtcaga atgaaggctg caaactcaaa gcagtagtgg 1440
85 aagctaagaa gttaactctg ggaggacttg aaaaagcaga gaaaaaagag gacaccagga 1500
86 tgtatctgct ggctttgaag aatgccctgc ttccagaagg catcccaagt cttctgaagt 1560
87 atgcagaagc aggagaaggg cccatcagcc acctggctac cactgctctc cagagatatg 1620
88 atctcccttt cataactgat gaggtgaaga agaccttaaa cagaatatac caccaaaacc 1680
89 gtaaagtcca tgaaaagact gtgcgcactg ctgcagctgc tatcatttta aataacaatc 1740
90 catcctacat ggacgtcaag aacatcctgc tgtctattgg ggagcttccc caagaaatga 1800
91 ataaatacat gctcgccatt gttcaagaca tcctacgttt ggaaatgcct gcaagcaaaa 1860
92 ttgtccgctg agttctgaag gaaatggtcg ctcaacaatta tgaccgtttc tccaggagtg 1920
93 gatcttcttc tgctacact ggctacatag aacgtagtcc ccgttcggca tctacttaca 1980
94 gcctagacat tctctactcg ggttctggca ttctaaggag aagtaacctg aacatctttc 2040
95 agtacattgg gaaggctggg cttcacggta gccagggtgg tattgaagcc caaggactgg 2100
96 aagccttaat cgcagccacc cctgacgagg gggaggagaa ccttgactcc tatgttggtg 2160
97 tgtcagccat cctctttgat gttcagctca gacctgtcac ctttttcaac ggatacagtg 2220
98 atttgatgtc caaaatgctg tcagcatctg gcgacctat cagtgtggtg aaaggactta 2280
99 ttctgctaata agatcattct caggaaactc agttacaatc tggactaaaa gccaatatag 2340
100 aggtccaggg tggctctagct attgatattt cagggtgcaat ggagtttagc ttgtggtatc 2400
101 gtgagtctaa aacccgagtg aaaaataggg tgactgtggt aataaccact gacatcacag 2460
102 tggactcttc ttttgtgaaa gctggcctgg aaaccagtac agaaacagaa gcaggcttgg 2520
103 agtttatctc cacagtgcag ttttctcagt acccattctt agtttgcag cagatggaca 2580
104 aggatgaagc tccattcagg caatttgaga aaaagtacga aaggctgtcc acaggcagag 2640
105 gttatgtctc tcagaaaaga aaagaaagcg tattagcagg atgtgaattc ccgctccatc 2700
106 aagagaactc agagatgtgc aaagtgggtg ttgccctca gccggatagt acttccagcg 2760
107 gatgggtttg aaactgacct gtgatatttt acttgaattt gtctccccga aagggaacaca 2820
108 atgtggcatg actaagtact tgctctctga gagcacagcg tttacatatt tacctgtatt 2880
109 taagattttt gtaaaaagct acaaaaaact gcagtttgat caaatttggg tatatgcagt 2940
110 atgctacca cagcgtcatt ttgaatcatc atgtgacgct ttcaacaacg ttcttagttt 3000
111 acttatacct ctctcaaata tcatttggtg cagtcagaat agttattctc taagaggaaa 3060
112 ctagtgtttg ttaaaaacaa aaataaaaaa aaaaccacac aaggagaacc caattttgtt 3120

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Input Set : A:\18989-033US.txt

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113 tcaacaattt ttgatcaatg tatatgaagc tcttgatagg acttccttaa gcatgacggg 3180
114 aaaaccaaac acgttcctta atcaggaaaa aaaaaaaaaa aaaaaagtaa gacacaaaca 3240
115 aaccattttt ttctcttttt ttggagttgg gggcccaggg agaagggaca aggcttttaa 3300
116 aagacttggt agccaacttc aagaattaat atttatgtct ctgttattgt tagttttaag 3360
117 ccttaaggta gaaggcacat agaaataaca tc 3392
120 <210> SEQ ID NO: 4
121 <211> LENGTH: 894
122 <212> TYPE: PRT
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 4
126 Met Ile Leu Leu Ala Val Leu Phe Leu Cys Phe Ile Ser Ser Tyr Ser
127 1 5 10 15
129 Ala Ser Val Lys Gly His Thr Thr Gly Leu Ser Leu Asn Asn Asp Arg
130 20 25 30
132 Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Leu Leu Asp Arg Gly Lys
133 35 40 45
135 Gly Lys Leu Gln Asp Ser Val Gly Tyr Arg Ile Ser Ser Asn Val Asp
136 50 55 60
138 Val Ala Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Gln Leu Ile
139 65 70 75 80
141 Gln Ile Thr Met Lys Asp Val Asn Val Glu Asn Val Asn Gln Gln Arg
142 85 90 95
144 Gly Glu Lys Ser Ile Phe Lys Gly Lys Ser Pro Ser Lys Ile Met Gly
145 100 105 110
147 Lys Glu Asn Leu Glu Ala Leu Gln Arg Pro Thr Leu Leu His Leu Ile
148 115 120 125
150 His Gly Lys Val Lys Glu Phe Tyr Ser Tyr Gln Asn Glu Ala Val Ala
151 130 135 140
153 Ile Glu Asn Ile Lys Arg Gly Leu Ala Ser Leu Phe Gln Thr Gln Leu
154 145 150 155 160
156 Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asn Cys Lys Val
157 165 170 175
159 Thr Tyr Gln Ala His Gln Asp Lys Val Ile Lys Ile Lys Ala Leu Asp
160 180 185 190
162 Ser Cys Lys Ile Ala Arg Ser Gly Phe Thr Thr Pro Asn Gln Val Leu
163 195 200 205
165 Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
166 210 215 220
168 Ser Phe Val Ile Ala Val Leu Ala Glu Glu Thr His Asn Phe Gly Leu
169 225 230 235 240
171 Asn Phe Leu Gln Thr Ile Lys Gly Lys Ile Val Ser Lys Gln Lys Leu
172 245 250 255
174 Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Leu Met Ser Gly Lys Gln
175 260 265 270
177 Ala Ala Ala Ile Ile Lys Ala Val Asp Ser Lys Tyr Thr Ala Ile Pro
178 275 280 285
180 Ile Val Gly Gln Val Phe Gln Ser His Cys Lys Gly Cys Pro Ser Leu
181 290 295 300
183 Ser Glu Leu Trp Arg Ser Thr Arg Lys Tyr Leu Gln Pro Asp Asn Leu

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184 305          310          315          320
186 Ser Lys Ala Glu Ala Val Arg Asn Phe Leu Ala Phe Ile Gln His Leu
187          325          330          335
189 Arg Thr Ala Lys Lys Glu Glu Ile Leu Gln Ile Leu Lys Met Glu Asn
190          340          345          350
192 Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr
193          355          360          365
195 Ser Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp
196          370          375          380
198 Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala
199 385          390          395          400
201 Ser His Pro Asn Glu Glu Leu Leu Arg Ala Leu Ile Ser Lys Phe Lys
202          405          410          415
204 Gly Ser Ile Gly Ser Ser Asp Ile Arg Glu Thr Val Met Ile Ile Thr
205          420          425          430
207 Gly Thr Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys
208          435          440          445
210 Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Ala
211          450          455          460
213 Glu Lys Lys Glu Asp Thr Arg Met Tyr Leu Leu Ala Leu Lys Asn Ala
214 465          470          475          480
216 Leu Leu Pro Glu Gly Ile Pro Ser Leu Leu Lys Tyr Ala Glu Ala Gly
217          485          490          495
219 Glu Gly Pro Ile Ser His Leu Ala Thr Thr Ala Leu Gln Arg Tyr Asp
220          500          505          510
222 Leu Pro Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr
223          515          520          525
225 His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Ala Ala Ala
226          530          535          540
228 Ala Ile Ile Leu Asn Asn Asn Pro Ser Tyr Met Asp Val Lys Asn Ile
229 545          550          555          560
231 Leu Leu Ser Ile Gly Glu Leu Pro Gln Glu Met Asn Lys Tyr Met Leu
232          565          570          575
234 Ala Ile Val Gln Asp Ile Leu Arg Leu Glu Met Pro Ala Ser Lys Ile
235          580          585          590
237 Val Arg Arg Val Leu Lys Glu Met Val Ala His Asn Tyr Asp Arg Phe
238          595          600          605
240 Ser Arg Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Ile Glu Arg Ser
241          610          615          620
243 Pro Arg Ser Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser
244 625          630          635          640
246 Gly Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Gly Lys
247          645          650          655
249 Ala Gly Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu
250          660          665          670
252 Ala Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser
253          675          680          685
255 Tyr Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val
256          690          695          700

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```

258 Thr Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala
259 705          710          715          720
261 Ser Gly Asp Pro Ile Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp
262          725          730          735
264 His Ser Gln Glu Leu Gln Leu Gln Ser Gly Leu Lys Ala Asn Ile Glu
265          740          745          750
267 Val Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ala Met Glu Phe Ser
268          755          760          765
270 Leu Trp Tyr Arg Glu Ser Lys Thr Arg Val Lys Asn Arg Val Thr Val
271          770          775          780
273 Val Ile Thr Thr Asp Ile Thr Val Asp Ser Ser Phe Val Lys Ala Gly
274 785          790          795          800
276 Leu Glu Thr Ser Thr Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr
277          805          810          815
279 Val Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys
280          820          825          830
282 Asp Glu Ala Pro Phe Arg Gln Phe Glu Lys Lys Tyr Glu Arg Leu Ser
283          835          840          845
285 Thr Gly Arg Gly Tyr Val Ser Gln Lys Arg Lys Glu Ser Val Leu Ala
286          850          855          860
288 Gly Cys Glu Phe Pro Leu His Gln Glu Asn Ser Glu Met Cys Lys Val
289 865          870          875          880
291 Val Phe Ala Pro Gln Pro Asp Ser Thr Ser Ser Gly Trp Phe
292          885          890
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 2878
297 <212> TYPE: DNA
298 <213> ORGANISM: Mus musculus
300 <400> SEQUENCE: 5
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302 tcctcctact ctgcttccgt taaaggtcac acaactggcc tctcattaaa taatgagcgg 120
303 ctatacaagc tcacgtactc cactgaagtg tttcttgatg ggggcaaagg aaaaccgcaa 180
304 gacagcgtgg gctacaaaat ctcatctgat gtggacgttg tgttactgtg gaggaatcct 240
305 gatggtgatg atgatcaagt gatccaagtc acgataacag ctgttaacgt tgaaaatgcg 300
306 ggtcaacaga gaggcgagaa gagcatcttc cagggcaaaa gtacacctaa gatcataggg 360
307 aaggacaacc tggaggctct gcagagaccc atgcttcttc atctggtccg ggggaagggtc 420
308 aaggagtctt actcctatga aaacgagcca gtgggcatag aaaatctcaa gagaggcttg 480
309 gctagcttat tccagatgca gctaagctct ggaactacca acgaggtaga tatctctggg 540
310 gattgtaaaag tgacctacca ggcccaacaa gacaaagtgg tcaaaattaa ggctctggat 600
311 acatgcaaaa ttgagcggtc tggatttaca acggcaaac aggtgctggg cgtcagttca 660
312 aaagccacat ctgtcactac ctacaagata gaggacagct ttgtaccgc tgtgcttgca 720
313 gaagagacca gggcttttgc cttgaacttc caacaaacca tagcaggaaa aatagtgtca 780
314 aagcagaaat tggagctgaa gacaactgaa gccggcccaa ggatgatccc cgggaagcaa 840
315 gtggcagggtg taattaaagc agttgattcc aaatacaaa ccattcccat tgtgggacag 900
316 gtcctcgagc gtgtctgcaa aggatgccct tctctggcgg agcactggaa gtccatcaga 960
317 aagaacctgg agcctgaaaa cctgtccaag gccgaggctg tccagagctt cctggccttc 1020
318 atccagcac cccggacttc gaggagagaa gagatcctcc agattctgaa ggcagagaag 1080
319 aaagaagtgc tccctcagct ggtggatgcc gtcacctctg ctcagactcc agactcgcta 1140
320 gaagccatcc tggacttttt ggatttcaaa agtgacagca gtatcatact ccaggaaagg 1200

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 22,23
Seq#:2; N Pos. 22,23
Seq#:11; Xaa Pos. 14,16,27,31,36,43,47,50,52,53,70,77,81,95,121,123,130,171
Seq#:11; Xaa Pos. 177,180,197,200,203,204,226,233,241,243,248,261
Seq#:12; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165
Seq#:12; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268
Seq#:12; Xaa Pos. 270,275,287
Seq#:13; Xaa Pos. 6,16,17,46,48,51,54,55,63,69,81,84,89,95,97,105,108,133
Seq#:13; Xaa Pos. 140,142,149,155,162,163,174,176,177,180,191,193,198,202
Seq#:14; Xaa Pos. 35,41,52,57,58,59,70,72,77,81,82,97,104,108,109,118,126
Seq#:14; Xaa Pos. 128,131,149,157,166,186,189,195,200,210,219,222,240,252
Seq#:14; Xaa Pos. 253,261,273,274,297
Seq#:15; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165
Seq#:15; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268
Seq#:15; Xaa Pos. 270,275,287
Seq#:16; Xaa Pos. 43,49,60,65,66,67,78,80,85,89,90,105,112,116,117,126,134
Seq#:16; Xaa Pos. 136,139,157,165,174,194,197,203,208,227,236,239,257,269
Seq#:16; Xaa Pos. 270,278,290,291,292,314

VARIABLE LOCATION SUMMARY

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Input Set : A:\18989-033US.txt

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Use of n's or Xaa's (NEW RULES):

Error Explanation: 2

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; N Pos. 22,23

Seq#:2; N Pos. 22,23

Seq#:11; Xaa Pos. 14,16,27,31,36,43,47,50,52,53,70,77,81,95,121,123,130,171

Seq#:11; Xaa Pos. 177,180,197,200,203,204,226,233,241,243,248,261

Seq#:12; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165

Seq#:12; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268

Seq#:12; Xaa Pos. 270,275,287

Seq#:13; Xaa Pos. 6,16,17,46,48,51,54,55,63,69,81,84,89,95,97,105,108,133

Seq#:13; Xaa Pos. 140,142,149,155,162,163,174,176,177,180,191,193,198,202

Seq#:14; Xaa Pos. 35,41,52,57,58,59,70,72,77,81,82,97,104,108,109,118,126

Seq#:14; Xaa Pos. 128,131,149,157,166,186,189,195,200,210,219,222,240,252

Seq#:14; Xaa Pos. 253,261,273,274,297

Seq#:15; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165

Seq#:15; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268

Seq#:15; Xaa Pos. 270,275,287

Seq#:16; Xaa Pos. 43,49,60,65,66,67,78,80,85,89,90,105,112,116,117,126,134

Seq#:16; Xaa Pos. 136,139,157,165,174,194,197,203,208,227,236,239,257,269

Seq#:16; Xaa Pos. 270,278,290,291,292,314

VERIFICATION SUMMARY

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Input Set : A:\18989-033US.txt

Output Set: N:\CRF4\10142004\J808052.raw

L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:52 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:2
L:52 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:2
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48
M:341 Repeated in SeqNo=12
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:32
M:341 Repeated in SeqNo=14
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48
M:341 Repeated in SeqNo=15
L:931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:32
M:341 Repeated in SeqNo=16